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Sequence Listing was accepted.

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Reviewer: Durreshwar Anjum

Timestamp: Tue Jun 12 14:01:41 EDT 2007

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Application No: 10565997 Version No: 1.0

Input Set:

Output Set:

Started: 2007-06-11 20:01:14.848
Finished: 2007-06-11 20:01:16.379
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 531 ms
Total Warnings: 32
Total Errors: 0
No. of SeqIDs Defined: 52
Actual SeqID Count: 52

Error code	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (21)
W 213	Artificial or Unknown found in <213> in SEQ ID (22)
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W 213	Artificial or Unknown found in <213> in SEQ ID (24)
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Input Set:

Output Set:

Started: 2007-06-11 20:01:14.848
Finished: 2007-06-11 20:01:16.379
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 531 ms
Total Warnings: 32
Total Errors: 0
No. of SeqIDs Defined: 52
Actual SeqID Count: 52

Error code	Error Description
	This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> NAGAI, RYOZO
MANABE, ICHIRO
ISHIHARA, ATSUSHI
TOTTORI, TSUNEAKI

<120> RNA CAPABLE OF SUPPRESSING EXPRESSION OF KLF5 GENE

<130> P29215

<140> 10565997
<141> 2007-06-11

<150> 10/565,997
<151> 2006-01-27

<150> PCT/JP04/11223
<151> 2004-07-29

<150> JP 2003-202863
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<150> JP 2004-075115
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<211> 19

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Synthetic oligonucleotide

<220>
<223> Description of Artificial Sequence: Synthetic
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<210> 18
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Synthetic oligonucleotide

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agggaggaag acguucaugt t 21

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<210> 20
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<210> 38

<211> 21
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<220>
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<210> 39
<211> 21
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<220>
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<210> 40
<211> 21
<212> RNA
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<220>
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<210> 41
<211> 20
<212> DNA
<213> Artificial Sequence

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<400> 41
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<210> 42
<211> 22
<212> DNA
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<220>

<223> Description of Artificial Sequence: Synthetic
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<400> 42
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22

<210> 43
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 43
ctccagcgac tcttgagat ag

22

<210> 44
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<212> DNA
<213> Artificial Sequence

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primer

<400> 44
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<210> 45
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<210> 46
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<222> (167)..(1504)

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gatcgcgatc gctccgtgtc ccgctcccgat aatccccaga ccgtcc atg ccc acg 175
Met Pro Thr
1

cgg gtg ctg acc atg agc gcc cgc ctg gga cca ctg ccc cag ccg ccg 223
Arg Val Leu Thr Met Ser Ala Arg Leu Gly Pro Leu Pro Gln Pro Pro
5 10 15

gcc gcg cag gcc gag ccc gtg ttc gcg cag ctc aag ccg gtg ctg ggc 271
Ala Ala Gln Ala Glu Pro Val Phe Ala Gln Leu Lys Pro Val Leu Gly
20 25 30 35

gct gcg aac ccg gcc cgc gac gcg gcg ctc ttc tcc gga gac gat ctg 319
Ala Ala Asn Pro Ala Arg Asp Ala Ala Leu Phe Ser Gly Asp Asp Leu
40 45 50

aaa cac gcg cac cac ccg cct gcg ccg cca gcc gct ggc ccg			367
Lys His Ala His His Pro Pro Ala Pro Pro Pro Ala Ala Gly Pro			
55	60	65	
cga ctg ccc tcg gag gag ctg gtc cag aca aga tgt gaa atg gag aag			415
Arg Leu Pro Ser Glu Glu Leu Val Gln Thr Arg Cys Glu Met Glu Lys			
70	75	80	
tat ctg acc cct cag ctc cct cca gtt ccg ata att tca gag cat aaa			463
Tyr Leu Thr Pro Gln Leu Pro Pro Val Pro Ile Ile Ser Glu His Lys			
85	90	95	
aag tat aga cga gac agt gcc tca gtg gta gac cag ttc ttc act gac			511
Lys Tyr Arg Arg Asp Ser Ala Ser Val Val Asp Gln Phe Phe Thr Asp			
100	105	110	115
act gaa ggc ata cct tac agc atc aac atg aac gtc ttc ctc cct gac			559
Thr Glu Gly Ile Pro Tyr Ser Ile Asn Met Asn Val Phe Leu Pro Asp			
120	125	130	
atc act cac ctg aga act ggc ctc tac aaa tcc cag aga cca tgc gta			607
Ile Thr His Leu Arg Thr Gly Leu Tyr Lys Ser Gln Arg Pro Cys Val			
135	140	145	
aca cag atc aag aca gaa cct gtt acc att ttc agc cac cag agc gag			655
Thr Gln Ile Lys Thr Glu Pro Val Thr Ile Phe Ser His Gln Ser Glu			
150	155	160	
tcg acg gcc cct cct cct ccg gcc ccc acc cag gct ctc ccc gag			703
Ser Thr Ala Pro Pro Pro Pro Ala Pro Thr Gln Ala Leu Pro Glu			
165	170	175	
ttc act agt atc ttc agc tcc cac cag acc aca gcg cca cca cag gag			751
Phe Thr Ser Ile Phe Ser Ser His Gln Thr Thr Ala Pro Pro Gln Glu			
180	185	190	195
gtg aac aat atc ttc atc aaa caa gaa ctt cct ata cca gat ctt cat			799
Val Asn Asn Ile Phe Ile Lys Gln Glu Leu Pro Ile Pro Asp Leu His			
200	205	210	
ctc tct gtc cct tcc cag cag ggc cac ctg tac cag ctg ttg aat aca			847
Leu Ser Val Pro Ser Gln Gln Gly His Leu Tyr Gln Leu Leu Asn Thr			
215	220	225	
ccg gat cta gac atg ccc agt tcg aca aac cag acg gca gta atg gac			895
Pro Asp Leu Asp Met Pro Ser Ser Thr Asn Gln Thr Ala Val Met Asp			
230	235	240	
acc ctt aat gtt tct atg gca ggc ctt aac cca cac ccc tct gct gtt			943
Thr Leu Asn Val Ser Met Ala Gly Leu Asn Pro His Pro Ser Ala Val			
245	250	255	
cca cag acg tca atg aaa cag ttc cag ggc atg ccc cct tgc acg tac			991
Pro Gln Thr Ser Met Lys Gln Phe Gln Gly Met Pro Pro Cys Thr Tyr			
260	265	270	275

acc atg cca agt cag ttt ctt cca cag cag gcc act tat ttt ccc ccg		1039	
Thr Met Pro Ser Gln Phe Leu Pro Gln Gln Ala Thr Tyr Phe Pro Pro			
280	285	290	
tca cca cca agc tca gag cct gga agt ccc gat aga caa gct gag atg		1087	
Ser Pro Pro Ser Ser Glu Pro Gly Ser Pro Asp Arg Gln Ala Glu Met			
295	300	305	
ctg cag aat ctc acc cca cct ccg tcc tat gcc gct aca att gct tcc		1135	
Leu Gln Asn Leu Thr Pro Pro Ser Tyr Ala Ala Thr Ile Ala Ser			
310	315	320	
aaa ctg gcg att cac aac cca aat tta cct gcc act ctg cca gtt aat		1183	
Lys Leu Ala Ile His Asn Pro Asn Leu Pro Ala Thr Leu Pro Val Asn			
325	330	335	
tcg cca act ctc cca cct gtc aga tac aac aga agg agt aac ccg gat		1231	
Ser Pro Thr Leu Pro Pro Val Arg Tyr Asn Arg Arg Ser Asn Pro Asp			
340	345	350	355
ctg gag aag cga cgt atc cac ttc tgc gat tat aat ggt tgc aca aaa		1279	
Leu Glu Lys Arg Arg Ile His Phe Cys Asp Tyr Asn Gly Cys Thr Lys			
360	365	370	
gtt tat aca aag tcg tct cac tta aaa gct cac ctg agg act cat acg		1327	
Val Tyr Thr Lys Ser Ser His Leu Lys Ala His Leu Arg Thr His Thr			
375	380	385	
ggc gag aag ccc tac aag tgc acc tgg gag ggc tgc gac tgg agg ttt		1375	
Gly Glu Lys Pro Tyr Lys Cys Thr Trp Glu Gly Cys Asp Trp Arg Phe			
390	395	400	
gcc cggtcg gat gag ctg acc cgc cac tac agg aag cac acg ggc gcc		1423	
Ala Arg Ser Asp Glu Leu Thr Arg His Tyr Arg Lys His Thr Gly Ala			
405	410	415	
aag ccg ttc cag tgc atg gtg tgc caa cgc agc ttc tcc cgc tcc gac		1471	
Lys Pro Phe Gln Cys Met Val Cys Gln Arg Ser Phe Ser Arg Ser Asp			
420	425	430	435
cac ctc gcg ctg cac atg aag cgc cac cag aac tgagcgagcg aacgctgcgc	1524		
His Leu Ala Leu His Met Lys Arg His Gln Asn			
440	445		
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taaaaaag		1591	

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<213> Homo sapiens

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<222> (312)..(1682)

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acgtgtggaa gagcggaaaga gttttgcctt tcgtgcgcgc cttcgaaaac tgccctgccgc 180

tgtctgagga gtccacccga aacctcccct cctccgcccgg cagccccgcg ctgagctcgc 240

cgaccacaagc cagcgtgggc gaggtggaa gtgcgcgcga cccgcgcctg gagctgcgc 300

cccgagtgcc c atg gct aca agg gtg ctg agc atg agc gcc cgc ctg gga 350

Met Ala Thr Arg Val Leu Ser Met Ser Ala Arg Leu Gly

1 5 10

ccc gtg ccc cag ccg ccg gcg ccg cag gac gag ccg gtg ttc gcg cag 398

Pro Val Pro Gln Pro Pro Ala Pro Gln Asp Glu Pro Val Phe Ala Gln

15 20 25

ctc aag ccg gtg ctg ggc gcc gcg aat ccg gcc cgc gac gcg gcg ctc 446

Leu Lys Pro Val Leu Gly Ala Ala Asn Pro Ala Arg Asp Ala Ala Leu

30 35 40 45

tcc ccc ggc gag gag ctg aag cac gcg cac cac cgc ccg cag gcg cag 494